BIOT TNOLOGY
 _rEMS
BRANCH

RECEIVED

#5
Dm J
6-14-0

2001
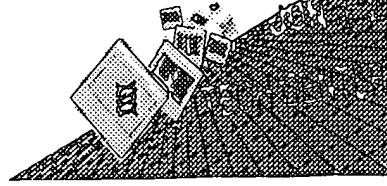
1600/2900

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/654, 652___

Source: ___1652___

Date Processed by STIC: ___5-29-01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: *09/654, 652*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
____Wrapped Aminos· was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
. prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
____Numbering use space characters, instead.

4____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
____"bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
____(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
____(NEW RULES) <210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
____(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
____Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11____Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
____"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1652

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/654,652   TIME: 15:26:36

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05292001\I654652.raw

Does Not Comply
Corrected Diskette Needed
PP 1-4

```
      4 <110> APPLICANT: Shyur, Lie-Fen
      5         Chen, Jui-Lin
      6         Yang, Ning-Sun
      9 <120> TITLE OF INVENTION: A Truncated Form of Fibrobacter Succinogenes 1,3-1,4-Beta-D-
Glucanase With
     10         Improved Enzymatic Activity And Thermo-Tolerance
W--> 11 <130> FILE REFERENCE: 4910-8
W--> 12 <140> CURRENT APPLICATION NUMBER: US 09/654,652
     13 <141> CURRENT FILING DATE: 2000-09-05
W--> 14 <150> PRIOR APPLICATION NUMBER:
W--> 15 <151> PRIOR FILING DATE:
E--> 16 <160> NUMBER OF SEQ ID: 6
```

Do not include headers which have no response.

↳ Number of sequences differ:
− 6 listed
− 10 shown

ERRORED SEQUENCES

```
     18 <210> SEQ ID NO: 1
     19 <211> LENGTH: 248
     20 <212> TYPE: PRT
     21 <213> ORGANISM: Artificial Sequence
W--> 22 <220> FEATURE:
     23 <223> OTHER INFORMATION: Modified enzyme with enhanced activity and thermal stability
W--> 24 <400> SEQUENCE: 1
     25 Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
E--> 26  1           5 .         10                15              20
     27 Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe
E--> 28      25        30    35                    40
     29 Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu
E--> 30              45      50    55        60
     31 Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
E--> 32      65              70                75    80
     33 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
E--> 34      85        90    95        100
     35 Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg
E--> 36      105       110   115       120
     37 Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu
E--> 38      125       130             135           140
     39 Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
E--> 40          145       150   155       160
     41 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser
E--> 42      165       170   175       180
     43 Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys
E--> 44      185       190   195       200
     45 Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg
E--> 46              205       210               215
E--> 47 220
     48 Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
E--> 49      225       230   235       240
```

Invalid Amino Acid numbering Use Spaces not Tabs. See #3 on the Error Summary Sheet.

```
      50 Pro Arg Asp Asp Glu Pro Ala Pro
E--> 51    245
      55 <210> SEQ ID NO: 2
      56 <211> LENGTH: 267
      57 <212> TYPE: PRT
      58 <213> ORGANISM: Artificial Sequence
W--> 59 <220> FEATURE:
      60 <223> OTHER INFORMATION: Modified enzyme with enhanced activity and thermal stability
W--> 61 <400> SEQUENCE: 2
      62 Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
E--> 63 1          5         10        15                  20
      64 Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe
E--> 65           25        30        35        40
      66 Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu
E--> 67              45        50        55        60
      68 Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
E--> 69    65        70        75        80
      70 Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
E--> 71           85        90        95        100
      72 Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg
E--> 73 105       110       115       120
      74 Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu
E--> 75    125                 130                 135                 140
      76 Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
E--> 77           145       150       155       160
      78 Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser
E--> 79 165       170       175       180
      80 Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys
E--> 81           185       190       195       200
      82 Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg
E--> 83                 205                 210       215       220
      84 Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
E--> 85    225       230       235       240
      86 Pro Arg Asp Asp Glu Pro Ala Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu
E--> 87    245       250       255       260
      88 Glu His His His His His His
E--> 89    265
      91 <210> SEQ ID NO: 3
      92 <211> LENGTH: 349
      93 <212> TYPE: PRT
      94 <213> ORGANISM: Fibrobacter succinogenes
W--> 95 <220> FEATURE:
      96 <223> OTHER INFORMATION:
W--> 97 <400> SEQUENCE: 3
      98 Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala Ala Ala Ala Ala
E--> 99 1          5         10        15        20
     100 Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu
E--> 101    25        30        35        40
     102 Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser
```

Invalid Amino Acid numbers See p.1

√

Invalid amino acid numbering.
See p.1

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/654,652   TIME: 15:26:36

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05292001\I654652.raw

```
E--> 103     45        50      55        60
    104 Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
E--> 105             65             70   75        80
    106 Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys
E--> 107     85      90      95      100
    108 Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala
E--> 109             105     110     115     120
    110 Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln
E--> 111   125     130     135     140
    112 Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
E--> 113                 145             150             155             160
    114 Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu
E--> 115         165     170             175     180
    116 Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu
E--> 117     185     190     195     200
    118 Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg
E--> 119 205     210     215     220
    120 Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
E--> 121 225     230     235     240
    122 Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn
E--> 123 245     250     255     260
    124 Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln Ser Ser Ser Ser Ala Pro Ala Ser
E--> 125 265     270     275     280
    126 Ser Ser Ser Val Pro Ala Ser Ser Ser Ser Val Pro Ala Ser Ser Ser Ser Ala Phe Val
E--> 127 285     290     295     300
    128 Pro Pro Ser Ser Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
E--> 129 305     310     315     320
    130 Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn Pro Asn Gly His
E--> 131 325     330     335     340
    132 Lys Arg Tyr Arg Val Asn Phe Glu His
E--> 133 345
    210 <210> SEQ ID NO: 7
    211 <211> LENGTH: (13)
    212 <212> TYPE: DNA
    213 <213> ORGANISM: Artificial Sequence
W--> 214 <220> FEATURE:
    215 <223> OTHER INFORMATION: PCR primer
W--> 216 <400> SEQUENCE: 7
E--> 217 tcaccaccat ggttagcgca aag          (13)
    219 <210> SEQ ID NO: 8
    220 <211> LENGTH: (15)
    221 <212> TYPE: DNA
    222 <213> ORGANISM: Artificial Sequence
W--> 223 <220> FEATURE:
    224 <223> OTHER INFORMATION: PCR primer
W--> 225 <400> SEQUENCE: 8
E--> 226 gccacgaatt ctgttcaaag ttcac         (15)
    228 <210> SEQ ID NO: 9
    229 <211> LENGTH: (17)
```

[handwritten annotations:]

Invalid amino acid numbering. See p. 1

Seq #7 — 13 listed — 23 shown

Seq #8 — 15 listed — 25 shown

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: **US/09/654,652**   TIME: 15:26:36

Input Set : **A:\PTO.txt**
Output Set: **C:\CRF3\05292001\I654652.raw**

```
        230 <212> TYPE: DNA
        231 <213> ORGANISM: Artificial Sequence
W-->    232 <220> FEATURE:
        233 <223> OTHER INFORMATION: PCR Primer
W-->    234 <400> SEQUENCE: 9
E-->    235 cagccggcga tggccatggt tagcgca        (17)
        237 <210> SEQ ID NO: 10
        238 <211> LENGTH: (19)
        239 <212> TYPE: DNA
        240 <213> ORGANISM: Artificial Sequence
W-->    241 <220> FEATURE:
        242 <223> OTHER INFORMATION: PCR Primer
W-->    243 <400> SEQUENCE: 10
E-->    244 ctgctagaag aattcggagc aggttcgtc        (19)
```

Seq #9
-17 listed
-27 shown

Seq #10
-19 listed
-29 shown

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/654,652**

DATE: 05/29/2001
TIME: 15:26:37

Input Set : **A:\PTO.txt**
Output Set: **C:\CRF3\05292001\I654652.raw**

```
L:11 M:283 W: Missing Blank Line separator, <130> field identifier
L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:14 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:16 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:26 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:28 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:30 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:32 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:34 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:36 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:38 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:40 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:42 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:46 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:47 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:49 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:59 M:283 W: Missing Blank Line separator, <220> field identifier
L:61 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:65 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:67 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:69 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:71 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:73 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:75 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:77 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:79 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:81 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:83 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:85 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:87 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:89 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:95 M:283 W: Missing Blank Line separator, <220> field identifier
L:97 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:101 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:103 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:105 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:107 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:109 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:111 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:113 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:115 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
```

Input Set : A:\PTO.txt
Output Set: C:\CRF3\05292001\I654652.raw

```
L:117 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:119 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:121 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:123 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:125 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:127 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:129 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:131 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:133 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:139 M:283 W: Missing Blank Line separator, <220> field identifier
L:141 M:283 W: Missing Blank Line separator, <400> field identifier
L:162 M:283 W: Missing Blank Line separator, <220> field identifier
L:164 M:283 W: Missing Blank Line separator, <400> field identifier
L:187 M:283 W: Missing Blank Line separator, <220> field identifier
L:189 M:283 W: Missing Blank Line separator, <400> field identifier
L:214 M:283 W: Missing Blank Line separator, <220> field identifier
L:216 M:283 W: Missing Blank Line separator, <400> field identifier
L:217 M:254 E: No. of Bases conflict, LENGTH:Input:13 Counted:23 SEQ:7
L:217 M:252 E: No. of Seq. differs, <211>LENGTH:Input:13 Found:23 SEQ:7
L:223 M:283 W: Missing Blank Line separator, <220> field identifier
L:225 M:283 W: Missing Blank Line separator, <400> field identifier
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:15 Counted:25 SEQ:8
L:226 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:25 SEQ:8
L:232 M:283 W: Missing Blank Line separator, <220> field identifier
L:234 M:283 W: Missing Blank Line separator, <400> field identifier
L:235 M:254 E: No. of Bases conflict, LENGTH:Input:17 Counted:27 SEQ:9
L:235 M:252 E: No. of Seq. differs, <211>LENGTH:Input:17 Found:27 SEQ:9
L:241 M:283 W: Missing Blank Line separator, <220> field identifier
L:243 M:283 W: Missing Blank Line separator, <400> field identifier
L:244 M:254 E: No. of Bases conflict, LENGTH:Input:19 Counted:29 SEQ:10
L:244 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:29 SEQ:10
L:16 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (10)
```